09/748,710.

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ		
L16	l14 and exon	0	L16
L15	L14 and bamh1	0	L15
L14	5866330.pn.	2	L14
L13	l11 and exon	1	L13
L12	L11 and bamH1	0	L12
L11	L10 and (serial analysis near5 gene expression$1)	2	L11
L10	(one base anchor$2 or single base anchor$2) near5 primer$1	12	L10
L9	l7 and exon	0	L9
L8	l7 and (one base anchor$2 or single base anchor$2)	0	L8
L7	L5 and ((restrict$3 or recognit$3) near5 BamH1)	1	L7
L6	L5 and ((recognition sequence or restrict$3) near5 end$1 near5 BAmH1)	0	L6
L5	serial analysis near5 gene expression	142	L5
L4	sage tag41	0	L4
L3	serial analysis of gene expression	0	L3
L2	sage	8162	L2
L1	serial analysis of gene expression	0	L1

END OF SEARCH HISTORY

End of Result Set

☐ Generate Collection

L7: Entry 1 of 1 File: USPT Oct 8, 2002

DOCUMENT-IDENTIFIER: US 6461814 B1
TITLE: Method of identifying gene transcription patterns

Brief Summary Text (11):
Recently, a variation of PCR for a random cDNA sequencing approach was described by Velculescu et al. (Velculescu, V. E. et al., Science 270:484 (1995)). This technique, called Serial Analysis of Gene Expression (SAGE), generates short, defined sequences from cDNAs which are randomly ligated in a tail-to-tail fashion and amplified by PCR to form "di-tags". These di-tags are then concatenated into arrays which are cloned and analyzed by DNA sequencing. Because each sequencing template contains identifiable tags corresponding to many genes, the potential throughput of SAGE exceeds traditional cDNA sequencing, allowing gene transcription profiling in many laboratories.

Brief Summary Text (29):
"A 5' cloning restriction endonuclease" as used herein, means a restriction endonuclease having a corresponding methylase or other protection means that can protect any DNA from cleavage by the enzyme. Preferably, the 5' cloning restriction endonuclease recognizes a sequence of between about four to ten bases. Examples of this most preferably, the 5' cloning restriction endonuclease is EcoRI, BamH1, HindIII

Other Reference Publication (49):
Velculescu et al., "Serial Analysis of Gene Expression," Science 270: 484-487, 1995.

09/748,710

* * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 12:13:29 ON 19 MAR 2003

=> file caplus medline biosis

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'CAPLUS' ENTERED AT 12:13:44 ON 19 MAR 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

FILE 'MEDLINE' ENTERED AT 12:13:44 ON 19 MAR 2003

FILE 'BIOSIS' ENTERED AT 12:13:44 ON 19 MAR 2003

=> s serial analysis gene expression#
L1 39 SERIAL ANALYSIS GENE EXPRESSION#

=> s l1 and bamH1 and exon
L2 0 L1 AND BAMH1 AND EXON

=> s l1 and exon
L3 1 L1 AND EXON

=> s l1 and bamH1
L4 0 L1 AND BAMH1

=> d l3 bib ab kwic

L3 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS
AN 2000:38520 CAPLUS
DN 132:203734
TI Generation of longer cDNA fragments from serial analysis of gene expression tags for gene identification
AU Chen, Jian-Jun; Rowley, Janet D.; Wang, San Ming
CS Section of Hematology/Oncology, University of Chicago Medical Center, Chicago, IL, 60637, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2000), 97(1), 349-353
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB A technique was developed called the generation of longer cDNA fragments from serial anal. of gene expression (SAGE) tags for gene identification (GLGI), to convert SAGE tags of 10 bases into their corresponding 3' cDNA fragments covering hundred bases. A primer contg. the 10-base SAGE tag is used as the sense primer, and a single base anchored oligo(dT) primer is used as an antisense primer in PCR, together with Pfu DNA polymerase. By using this approach, a cDNA fragment extending from the SAGE tag toward the 3' end of the corresponding sequence can be generated. Application of the GLGI technique can solve 2 crit. issues in applying the SAGE technique: one is that a longer fragment corresponding to a SAGE tag, which has no match in databases, can be generated for further studies; the other is that the specific fragment corresponding to a SAGE tag can be identified from multiple sequences that match the same SAGE tag. The development of the GLGI method provides several potential applications.

First, it provides a strategy for even wider application of the SAGE technique for quant. anal. of global gene expression. Second, a combined application of SAGE/GLGI can be used to complete the catalog of the expressed genes in human and in other eukaryotic species. Third, it can be used to identify the 3' cDNA sequence from any **exon** within a gene. It can also be used to confirm the reality of exons predicted by bioinformatic tools in genomic sequences. Fourth, a combined application of SAGE/GLGI can be applied to define the 3' boundary of expressed genes in the genomic sequences in human and in other eukaryotic genomes.

RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB A technique was developed called the generation of longer cDNA fragments from serial anal. of gene expression (SAGE) tags for gene identification (GLGI), to convert SAGE tags of 10 bases into their corresponding 3' cDNA fragments covering hundred bases. A primer contg. the 10-base SAGE tag is used as the sense primer, and a single base anchored oligo(dT) primer is used as an antisense primer in PCR, together with Pfu DNA polymerase. By using this approach, a cDNA fragment extending from the SAGE tag toward the 3' end of the corresponding sequence can be generated. Application of the GLGI technique can solve 2 crit. issues in applying the SAGE technique: one is that a longer fragment corresponding to a SAGE tag, which has no match in databases, can be generated for further studies; the other is that the specific fragment corresponding to a SAGE tag can be identified from multiple sequences that match the same SAGE tag. The development of the GLGI method provides several potential applications. First, it provides a strategy for even wider application of the SAGE technique for quant. anal. of global gene expression. Second, a combined application of SAGE/GLGI can be used to complete the catalog of the expressed genes in human and in other eukaryotic species. Third, it can be used to identify the 3' cDNA sequence from any **exon** within a gene. It can also be used to confirm the reality of exons predicted by bioinformatic tools in genomic sequences. Fourth, a combined application of SAGE/GLGI can be applied to define the 3' boundary of expressed genes in the genomic sequences in human and in other eukaryotic genomes.

ST cDNA generation SAGE tag gene identification; **serial analysis gene expression** cDNA generation; GLGI cDNA generation **serial analysis gene expression**

```
=> s pattern# (10a) gene transcription#
L5          369 PATTERN# (10A) GENE TRANSCRIPTION#

=> s l5 and gene expression#
   1 FILES SEARCHED...
L6          177 L5 AND GENE EXPRESSION#

=> s l6 and exon#
L7            3 L6 AND EXON#

=> s l7 and BamH1
L8            0 L7 AND BAMH1

=> dup rem l7
PROCESSING COMPLETED FOR L7
L9            2 DUP REM L7 (1 DUPLICATE REMOVED)

=> d l9 1-2 bib ab kwic

L9   ANSWER 1 OF 2     MEDLINE
AN   97211325      MEDLINE
DN   97211325   PubMed ID: 9058323
TI   Elements between the protein-coding regions of the adjacent beta 4 and
     alpha 3 acetylcholine receptor genes direct neuron-specific expression in
```

the central nervous system.

AU Yang X; Yang F; Fyodorov D; Wang F; McDonough J; Herrup K; Deneris E

CS Department of Neurosciences, Case Western Reserve University School of Medicine, Cleveland, Ohio 44106-4975, USA.

NC NS18381 (NINDS)
NS29123 (NINDS)

SO JOURNAL OF NEUROBIOLOGY, (1997 Mar) 32 (3) 311-24.
Journal code: 0213640. ISSN: 0022-3034.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199706

ED Entered STN: 19970620
Last Updated on STN: 19970620
Entered Medline: 19970612

AB The expression patterns of three clustered neuronal nicotinic acetylcholine receptor (nAchR) subunit genes ordered beta 4, alpha 3, and alpha 5 overlap extensively in the peripheral nervous system (PNS) but only partially in the central nervous system (CNS). We have begun to investigate cell type-specific cis elements regulating these genes by analyzing in both cell culture and transgenic mice, a 2.8-kb fragment (-2732/+47) containing the alpha 3 promoter region, the beta 4/alpha 3 intergenic region, and a portion of the beta 4 3'-untranslated **exon**. The -2732/+47 fragment is preferentially active in PC12 cells relative to nonneural cell lines. Deletion analysis revealed a cell type-specific positive transcriptional element positioned in the beta 4 3'-untranslated **exon**. The positive element is likely to be an enhancer and not a second alpha 3 promoter, because no alpha 3 **exons** are present in this region. Having shown in cell culture that cell-type specific cis elements are positioned between the beta 4 and alpha 3 coding regions, we investigated the activity of -2732/+47 in vivo. Transgenic mice were generated, which carry the lacZ gene fused downstream of -2732/+47. Expression of the lacZ transgene is restricted to neurons of the CNS; no expression was detected in the PNS or in nonneural tissues. LacZ-positive cells were detected virtually exclusively in a subset of CNS nuclei that transcribe the endogenous alpha 3 gene. Some overlap was seen with the beta 4 gene, but nearly none with the alpha 5 gene. Our results demonstrate that cis elements positioned between the alpha 3 and beta 4 coding regions are important for establishing part of the restricted CNS **patterns** of beta 4, alpha 3, and alpha 5 **gene transcription**.

AB . . . containing the alpha 3 promoter region, the beta 4/alpha 3 intergenic region, and a portion of the beta 4 3'-untranslated **exon**. The -2732/+47 fragment is preferentially active in PC12 cells relative to nonneural cell lines. Deletion analysis revealed a cell type-specific positive transcriptional element positioned in the beta 4 3'-untranslated **exon**. The positive element is likely to be an enhancer and not a second alpha 3 promoter, because no alpha 3 **exons** are present in this region. Having shown in cell culture that cell-type specific cis elements are positioned between the beta. . . elements positioned between the alpha 3 and beta 4 coding regions are important for establishing part of the restricted CNS **patterns** of beta 4, alpha 3, and alpha 5 **gene transcription**.

CT Check Tags: Animal; Support, U.S. Gov't, P.H.S.
Central Nervous System: CY, cytology
*Central Nervous System: ME, metabolism
Exons
Gene Expression
*Genes
Genes, Reporter
Mice
Mice, Transgenic
*Neurons: ME, metabolism

PC12 Cells
Promoter Regions (Genetics)
Rats
*Receptors, Nicotinic: GE,. . .

L9 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
AN 1992:209024 CAPLUS
DN 116:209024
TI K-ras **gene expression** in the regenerating rat liver
AU Park, Sun Hee; Lee, Seung Ki; Park, Jong Sang
CS Coll. Nat. Sci., Seoul Natl. Univ., Seoul, 151-742, S. Korea
SO Han'guk Saenghwa Hakhoechi (1992), 25(1), 9-13
CODEN: KBCJAK; ISSN: 0368-4881
DT Journal
LA Korean
AB K-ras **Gene expression** in the regenerating liver after partial hepatectomy was tested by using dot hybridization. K-ras **Gene transcription** after the partial hepatectomy is amplified and its RNA splicing **pattern** is changed. In normal liver **exon** 4a is spliced out and only K-ras proteins contg. **exon** 4b are produced. In regenerating liver **exon** 4b is spliced out and K-ras proteins contg. **exon** 4a may be formed at a frequencey 1000%-fold that in normal liver.
TI K-ras **gene expression** in the regenerating rat liver
AB K-ras **Gene expression** in the regenerating liver after partial hepatectomy was tested by using dot hybridization. K-ras **Gene transcription** after the partial hepatectomy is amplified and its RNA splicing **pattern** is changed. In normal liver **exon** 4a is spliced out and only K-ras proteins contg. **exon** 4b are produced. In regenerating liver **exon** 4b is spliced out and K-ras proteins contg. **exon** 4a may be formed at a frequencey 1000%-fold that in normal liver.
ST rat regenerating liver gene Kras transcription; **exon** Kras protein regenerating rat liver
IT Ribonucleic acids, messenger
RL: BIOL (Biological study)
(for gene K-ras protein, in regenerating rat liver, **exon** 4a in)
IT Transcription, genetic
(of gene K-ras, in regenerating rat liver, **exon** 4a in relation to)
IT Rat
(regenerating liver of, gene K-ras transcription in, **exon** 4a in relation to)
IT Liver, metabolism
(regenerating, of rat, gene K-ras transcription in, **exon** 4a in relation to)
IT Genetic element
RL: BIOL (Biological study)
(**exon**, 4a, in gene K-ras mRNA, in regenerating rat liver, **exon** 4b splicing in relation to)
IT G proteins (guanine nucleotide-binding proteins)
RL: BIOL (Biological study)
(p21v-Ki-ras, in regenerating rat liver, **exon** 4a in mRNA for)
IT Gene, animal
RL: BIOL (Biological study)
(c-Ki-ras, transcription of, in regenerating rat liver, **exon** 4a in relation to)

=> s hodgkin cell#
L10 393 HODGKIN CELL#

=>

=> d l10 393 kwic

L10 ANSWER 393 OF 393 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
IT Miscellaneous Descriptors
ABSTRACT HUMAN MALIGNANT LYMPHOMA **HODGKIN CELLS**
STEINBERGS GIANT CELLS

=> d l10 1 kwic

L10 ANSWER 1 OF 393 CAPLUS COPYRIGHT 2003 ACS
IT Hodgkin's disease
(**Hodgkin cell**; loss of B-lineage-specific gene
expression program in Hodgkin and Reed-Sternberg cells of Hodgkin's
lymphoma)

=>